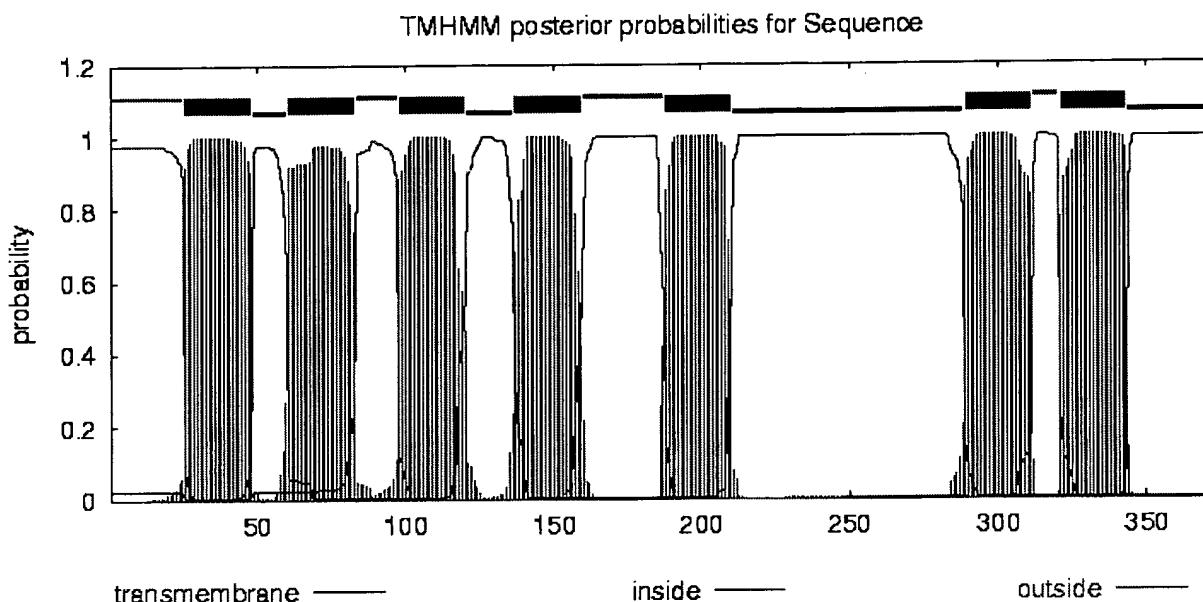


## APPENDIX 2



### A. TMHMM result HELP with output formats

---

```
# Sequence Length: 373
# Sequence Number of predicted TMHs: 7
# Sequence Exp number of AAs in TMHs: 156.69396
# Sequence Exp number, first 60 AAs: 23.36212
# Sequence Total prob of N-in: 0.02414
# Sequence POSSIBLE N-term signal sequence
Sequence      TMHMM2.0      outside      1      25
Sequence      TMHMM2.0      TMhelix     26      48
Sequence      TMHMM2.0      inside       49      60
Sequence      TMHMM2.0      TMhelix     61      83
Sequence      TMHMM2.0      outside     84      97
Sequence      TMHMM2.0      TMhelix     98     120
Sequence      TMHMM2.0      inside      121     136
Sequence      TMHMM2.0      TMhelix     137     159
Sequence      TMHMM2.0      outside     160     187
Sequence      TMHMM2.0      TMhelix     188     210
Sequence      TMHMM2.0      inside      211     288
Sequence      TMHMM2.0      TMhelix     289     311
Sequence      TMHMM2.0      outside     312     320
Sequence      TMHMM2.0      TMhelix     321     343
Sequence      TMHMM2.0      inside      344     373
```

---

```
# plot in postscript, script for making the plot in gnuplot, data for plot
```

## Conserved Tryptophan and Proline in TM6

### GPCR

hARE-2  
ghrelin receptor  
CXCR3 chemokine receptor  
5-hydroxytryptamine (serotonin) receptor 2A  
5-hydroxytryptamine (serotonin) receptor 2B  
5-hydroxytryptamine (serotonin) receptor 2C  
dopamine receptor D3  
dopamine receptor D1  
histamine receptor H3  
galanin receptor 1  
neuropeptide Y receptor Y1  
neurotensin receptor 1  
melanocortin 4 receptor  
adenosine A1 receptor  
cannabinoid receptor 1

### TM6 as predicted by TMHMM

YAITLLFLLLWSPYIVACYWRVF  
MLAVVVFAFILCWLPFHVGRLF  
LVVVVVVVAFALCWTPYHLVV  
LGIVFFLFVVMWCPFFITNIMAV  
GIVFFLFLLMWCPFFITNITLVL  
VLGIVFFVFLIMWCPFFITNILS  
VAIVLGAFIVCWLPFFLTHVLNT  
TLSVIMGVFVCCWLPPFILNCIL  
AVIVSIFGLCWAPYTLLMIIRAA  
TVLVVVVVFGISWLPHIIHLWA  
IMLLSIVVAFAVCWLPLTIFNTV  
VLRAVVIASFVVCWLPHYHVRRLMF  
ITLTILIGVFVVCWAPFFLHLIF  
LALILFLFALSWLPLHILNCITL  
LVLILVVLIIICWGPLLAIMVYDV